STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/595,562_
Source: _IFWP_
Date Processed by STIC: _2/1/07_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER
VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission
   User Manual - ePAVE**)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/595,562_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino . The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering use space characters, instead.

4_____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length Sequence(s) _1,2,3,56,61,69_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11_____Use of <220> Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12_____PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

Please consult Sequence Rules for VALID format (handwritten)

IFWP

(barcode)

RAW SEQUENCE LISTING   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:51

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

Does Not Comply Corrected Diskette Needed (stamp)

see pp 1-9 (handwritten)

```
   3 <110> APPLICANT: Medvet Science, Pty Ltd
   4        Guthridge, Mark
   5        Ramshaw, Hayley
   6        Stomski, Frank
   7        Felquer, Fernando
   8        Lopez, Angel
  10 <120> TITLE OF INVENTION: A Bidentate Motif and Methods of Use
W--> 12 <130> FILE REFERENCE:
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/595,562
C--> 14 <141> CURRENT FILING DATE: 2006-04-27
  14 <160> NUMBER OF SEQ ID NOS: 71
  16 <170> SOFTWARE: PatentIn version 3.3
```

insert this mandatory numeric identifier and response (handwritten)

ERRORED SEQUENCES

```
  18 <210> SEQ ID NO: 1        <211> 10  (handwritten)
  19 <212> TYPE: PRT
  20 <213> ORGANISM: Homo sapiens
  23 <220> FEATURE:
  24 <221> NAME/KEY: misc_feature
  25 <222> LOCATION: (2)..(3)
  26 <223> OTHER INFORMATION: Xaa can be any residue
  28 <220> FEATURE:
  29 <221> NAME/KEY: misc_feature
  30 <222> LOCATION: (5)..(5)
  31 <223> OTHER INFORMATION: Xaa (1-13 repeats) can be any residue
  33 <220> FEATURE:
  34 <221> NAME/KEY: misc_feature
  35 <222> LOCATION: (6)..(6)
  36 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
  38 <220> FEATURE:
  39 <221> NAME/KEY: misc_feature
  40 <222> LOCATION: (7)..(7)
  41 <223> OTHER INFORMATION: Xaa (2-3 repeats) can be any residue or a hydrophobic residue
or an
  42        equivalent thereof
  44 <220> FEATURE:
  45 <221> NAME/KEY: misc_feature
  46 <222> LOCATION: (8)..(8)
  47 <223> OTHER INFORMATION: Xaa is serine or threonine
  49 <220> FEATURE:
  50 <221> NAME/KEY: misc_feature
  51 <222> LOCATION: (9)..(9)
```

variable length is) not permitted — see item 5 on Error summary sheet (handwritten)

see item 5 on Error summary sheet (handwritten)

RAW SEQUENCE LISTING   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:51

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

```
 52 <223> OTHER INFORMATION: Xaa can be any residue

      54 <400> SEQUENCE: 1
W-->  56 Asn Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Pro
E-->  57 1               5                10
      60 <210> SEQ ID NO: 2
      61 <212> TYPE: PRT
      62 <213> ORGANISM: Homo sapiens
      65 <220> FEATURE:
      66 <221> NAME/KEY: misc_feature
      67 <222> LOCATION: (2)..(2)
      68 <223> OTHER INFORMATION: Xaa (1-16 repeats) can be any residue
      70 <220> FEATURE:
      71 <221> NAME/KEY: misc_feature
      72 <222> LOCATION: (3)..(3)
      73 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
      75 <220> FEATURE:
      76 <221> NAME/KEY: misc_feature
      77 <222> LOCATION: (4)..(4)
      78 <223> OTHER INFORMATION: Xaa (2-3 repeats) can be any residue or a hydrophobic residue
or an
      79        equivalent thereof
      81 <220> FEATURE:
      82 <221> NAME/KEY: misc_feature
      83 <222> LOCATION: (5)..(5)
      84 <223> OTHER INFORMATION: Xaa is serine or threonine
      86 <220> FEATURE:
      87 <221> NAME/KEY: misc_feature
      88 <222> LOCATION: (6)..(6)
      89 <223> OTHER INFORMATION: Xaa can be any residue

      92 <400> SEQUENCE: 2
W-->  94 Tyr Xaa Xaa Xaa Xaa Xaa Pro
E-->  95 1               5
      98 <210> SEQ ID NO: 3
      99 <212> TYPE: PRT
     100 <213> ORGANISM: Homo sapiens
     103 <220> FEATURE:
     104 <221> NAME/KEY: misc_feature
     105 <222> LOCATION: (2)..(3)
     106 <223> OTHER INFORMATION: Xaa can be any residue
     108 <220> FEATURE:
     109 <221> NAME/KEY: misc_feature
     110 <222> LOCATION: (4)..(4)
     111 <223> OTHER INFORMATION: Tyr is phosphotyrosine
     113 <220> FEATURE:
     114 <221> NAME/KEY: misc_feature
     115 <222> LOCATION: (5)..(5)
     116 <223> OTHER INFORMATION: Xaa (1-30 repeats) can be any residue
     118 <220> FEATURE:
```

[handwritten annotations: "insert this mandatory numeric identifier", "<211>", "see item 5", "see item 5", "<211>"]

RAW SEQUENCE LISTING   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:51

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

```
      119 <221> NAME/KEY: misc_feature
      120 <222> LOCATION: (6)..(6)
      121 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
      123 <220> FEATURE:
      124 <221> NAME/KEY: misc_feature
      125 <222> LOCATION: (7)..(7)
      126 <223> OTHER INFORMATION: Xaa (1-4 repeats) can be any residue
      128 <220> FEATURE:
      129 <221> NAME/KEY: misc_feature
      130 <222> LOCATION: (8)..(8)
      131 <223> OTHER INFORMATION: Xaa is phosphoserine or phosphothreonine
      133 <220> FEATURE:
      134 <221> NAME/KEY: misc_feature
      135 <222> LOCATION: (9)..(9)
      136 <223> OTHER INFORMATION: Xaa can be any residue

      138 <400> SEQUENCE: 3
W--> 140 Asn Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa
E--> 141 1               5
      144 <210> SEQ ID NO: 4
      145 <212> TYPE: PRT
      146 <213> ORGANISM: Homo sapiens

      148 <400> SEQUENCE: 4
E--> 150 Asn Gly Pro Tyr Leu Gly....... Pro Pro... His Ser Arg Ser Leu Pro
E--> 151 1               5                              10
      154 <210> SEQ ID NO: 5
      155 <212> TYPE: PRT
      156 <213> ORGANISM: Homo sapiens

      158 <400> SEQUENCE: 5
E--> 160 Asn Val His Tyr Arg Thr....... Pro.... Lys Thr His Thr Met Pro
E--> 161 1               5                              10
      164 <210> SEQ ID NO: 6
      165 <212> TYPE: PRT
      166 <213> ORGANISM: Homo sapiens

      168 <400> SEQUENCE: 6
E--> 170 (*)Arg Tyr Phe Thr Gln Lys Glu Glu....... Thr Glu Ser Gly Ser Gly Pro
E--> 171 1               5                              10               15
      174 <210> SEQ ID NO: 7
      175 <212> TYPE: PRT
      176 <213> ORGANISM: Homo sapiens

      178 <400> SEQUENCE: 7
E--> 180 Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu.... Pro... Arg Tyr
      181 1               5                   10                        15
E--> 184 Arg Ser Val Ser Glu Pro
      188 <210> SEQ ID NO: 8
```

[Handwritten annotations:]
these are invalid. If you are denoting a gap, delete the 2 Pro's, and begin a new SEQ ID NO with this group. Otherwise, number the amino acids.
same error
same error
same error
delete # K

‹2117 13

```
     189 <212> TYPE: PRT
     190 <213> ORGANISM: Homo sapiens

     192 <400> SEQUENCE: 8
E--> 194 Asn Pro Thr Tyr Ser Val Met(........)Arg Ser His Ser Tyr Pro
E--> 195 1              5                           10
     198 <210> SEQ ID NO: 9  )‹2117 24
     199 <212> TYPE: PRT
     200 <213> ORGANISM: Homo sapiens

     202 <400> SEQUENCE: 9
E--> 204 Asn Ile Phe Tyr Leu Ile Arg(........)Lys Ser Gly Ser Phe Pro Met Pro Glu
E--> 205 1              5                           10                      15
E--> 208 Leu Lys Leu Ser Ile Ser Phe Pro
     212 <210> SEQ ID NO: 10    )‹2117 19
     213 <212> TYPE: PRT
     214 <213> ORGANISM: Homo sapiens

     216 <400> SEQUENCE: 10
E--> 218 Asn Glu Glu Tyr Leu Asp Leu Ser Gln(......)Pro Leu Glu Gln Tyr Ser Pro
E--> 219 1              5                             10                    15
E--> 222 Ser Tyr Pro
     226 <210> SEQ ID NO: 11   )‹2117 19
     227 <212> TYPE: PRT
     228 <213> ORGANISM: Homo sapiens

     230 <400> SEQUENCE: 11
E--> 232 Asn Gln Glu Tyr Leu Asp Leu Ser Met(........)Pro Leu Asp Gln Tyr Ser Pro
E--> 233 1              5                               10                   15
E--> 236 Ser Phe Pro
     240 <210> SEQ ID NO: 12   )‹2117 16
     241 <212> TYPE: PRT
     242 <213> ORGANISM: Homo sapiens

     244 <400> SEQUENCE: 12
E--> 246 Asn Ala Thr Tyr Lys Val Asp(.........)Val Ile Gln Arg Thr Arg Ser Lys Pro
E--> 247 1              5                         10                      15
     250 <210> SEQ ID NO: 13   )‹2117 11
     251 <212> TYPE: PRT
     252 <213> ORGANISM: Homo sapiens

     254 <400> SEQUENCE: 13
E--> 256 Asn Pro Glu Tyr(........)His Ser Ala Ser Ser Gly Pro
E--> 257 1              5                        10
     260 <210> SEQ ID NO: 14   )‹2117 10
     261 <212> TYPE: PRT
     262 <213> ORGANISM: Homo sapiens

     264 <400> SEQUENCE: 14
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/595,562

DATE: 02/01/2007
TIME: 12:08:51

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

```
E--> 266 Asn Pro Asp Tyr(..........Trp Asn His Ser Leu Pro
E--> 267 1                          5                  10
     270 <210> SEQ ID NO: 15      <211723
     271 <212> TYPE: PRT
     272 <213> ORGANISM: Homo sapiens

     274 <400> SEQUENCE: 15
E--> 276 Asn Pro Ser Tyr Ser Ser Asn Pro Phe Val Asn Tyr Asn(.......)Lys Thr Ser
E--> 277 1               5                  10                         15
E--> 280 Ile Cys Ser Lys Ser Asn Pro
     284 <210> SEQ ID NO: 16      20     <211711
     285 <212> TYPE: PRT
     286 <213> ORGANISM: Homo sapiens

     288 <400> SEQUENCE: 16
E--> 290 Asn Thr Leu Tyr(..............)Phe Asn Ser Gln Ser Ser Pro
E--> 291 1                          5                  10
     294 <210> SEQ ID NO: 17      <211724
     295 <212> TYPE: PRT
     296 <213> ORGANISM: Homo sapiens

     298 <400> SEQUENCE: 17
E--> 300 Asn Pro Val Tyr Gln Lys Thr Thr Glu Asp Glu Val His Ile(....)Cys His
E--> 301 1               5                  10                         15
E--> 304 Asn Gln Asp Gly Tyr Ser Tyr Pro
     308 <210> SEQ ID NO: 18      20     <211724
     309 <212> TYPE: PRT
     310 <213> ORGANISM: Homo sapiens

     312 <400> SEQUENCE: 18
     314 Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp Ile
     315 1               5                  10                  15
E--> 318 Gly(..)Arg His(...)Ser Ala Ser Val Gly
     341 <210> SEQ ID NO: 20   20
     342 <212> TYPE: PRT
     343 <213> ORGANISM: Homo sapiens
E--> 345 <211> LENGTH:
     345 <400> SEQUENCE: 20
E--> 347 Asn Pro Ile Tyr..............Lys Ser Ala Val Thr Thr Val Val
E--> 348 1
     351 <210> SEQ ID NO: 21
     352 <212> TYPE: PRT
     353 <213> ORGANISM: Homo sapiens
E--> 355 <211> LENGTH:
     355 <400> SEQUENCE: 21
E--> 357 Asn Pro Leu Tyr..............Lys Ser Ala Ile Thr Thr Thr Val
E--> 358 1
     361 <210> SEQ ID NO: 22
     362 <212> TYPE: PRT
```

same error as above

```
      363 <213> ORGANISM: Homo sapiens
E--> 365 <211> LENGTH:
      365 <400> SEQUENCE: 22
E--> 367 Asn Pro Leu Tyr..............Lys Glu Ala Thr Ser Thr Phe Thr
E--> 368 1
      371 <210> SEQ ID NO: 23
      372 <212> TYPE: PRT
      373 <213> ORGANISM: Homo sapiens
E--> 375 <211> LENGTH:
      375 <400> SEQUENCE: 23
E--> 377 Asn Pro Leu Tyr..............Arg Lys Pro Ile Ser Thr His Thr
E--> 378 1
      381 <210> SEQ ID NO: 24
      382 <212> TYPE: PRT
      383 <213> ORGANISM: Homo sapiens
E--> 385 <211> LENGTH:
      385 <400> SEQUENCE: 24
E--> 387 Asn Pro Leu Tyr..............Arg Gly Ser Thr Ser Thr Phe Lys
E--> 388 1
      391 <210> SEQ ID NO: 25
      392 <212> TYPE: PRT
      393 <213> ORGANISM: Homo sapiens
E--> 395 <211> LENGTH:
      395 <400> SEQUENCE: 25
E--> 397 Pro Gly His Tyr Leu.............Arg Cys Asp Ser Thr Gln Pro
E--> 398 1               5
      421 <210> SEQ ID NO: 28
      422 <212> TYPE: PRT
      423 <213> ORGANISM: Homo sapiens
E--> 425 <211> LENGTH:
      425 <400> SEQUENCE: 28
E--> 427 His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe...............Ser Arg
E--> 428 1               5                    10
E--> 431 Ser Glu Ser Thr Gln Pro
      435 <210> SEQ ID NO: 29
      436 <212> TYPE: PRT
      437 <213> ORGANISM: Homo sapiens
E--> 439 <211> LENGTH:
      439 <400> SEQUENCE: 29
E--> 441 Trp Lys Met Tyr Glu Val Tyr Asp Ala.......Lys Ser Lys Ser Val Ser Leu
E--> 442 1               5
E--> 445 Pro
      502 <210> SEQ ID NO: 34
      503 <212> TYPE: PRT
      504 <213> ORGANISM: Homo sapiens
E--> 506 <211> LENGTH:
      506 <400> SEQUENCE: 34
E--> 508 Glu Glu Ile Tyr Ile Ile Met....................Gln Ser Cys Trp Ala Phe Asp Ser
E--> 509 Arg
```

global error

same error in seqs. 26,27

same error in seqs. 30-32

same error in seqs. 35-39

```
                    RAW SEQUENCE LISTING          DATE: 02/01/2007
                    PATENT APPLICATION:  US/10/595,562    TIME: 12:08:51

                    Input Set : A:\PTO.SS.TXT
                    Output Set: N:\CRF4\02012007\J595562.raw

E--> 510 1                 5
E--> 513 Lys Arg Pro Ser Phe Pro
     547 <210> SEQ ID NO: 38
     548 <212> TYPE: PRT
     549 <213> ORGANISM: Homo sapiens
E--> 551 <211> LENGTH:
     551 <400> SEQUENCE: 38
E--> 553 Leu Val Ala Tyr Ile Ala Phe Lys Arg Trp Asn Ser Cys Lys Gln Asn.........
     554 1                 5                 10              15
E--> 557 .......Lys Gln Gly Ala Asn Ser Arg Pro Val Asn Gln Thr Pro Pro Pro Glu
E--> 561 Gly Glu Lys Leu His Ser Asp Ser Gly Ile Ser
     584 <210> SEQ ID NO: 41
     585 <212> TYPE: PRT
     586 <213> ORGANISM: Homo sapiens
E--> 588 <211> LENGTH:
     588 <400> SEQUENCE: 41
     590 Asn Pro Asn Tyr Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro
E--> 591 1                 5     10      10     15        15
E--> 594 Trp Thr.................Lys Val Phe Lys Ser Arg Thr Pro Pro
     650 <210> SEQ ID NO: 46        20                 25
     651 <212> TYPE: PRT
     652 <213> ORGANISM: Homo sapiens
E--> 654 <211> LENGTH:
     654 <400> SEQUENCE: 46
E--> 656 Asn Gln Glu Tyr...........Leu Asp Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro
E--> 657 1
E--> 660 Ser Phe Pro
     664 <210> SEQ ID NO: 47
     665 <212> TYPE: PRT
     666 <213> ORGANISM: Homo sapiens
E--> 668 <211> LENGTH:
     668 <400> SEQUENCE: 47
E--> 670 Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu..............Gln Tyr Ser Pro
E--> 671 1                 5                 10
E--> 674 Ser Tyr
     678 <210> SEQ ID NO: 48
     679 <212> TYPE: PRT
     680 <213> ORGANISM: Homo sapiens
E--> 682 <211> LENGTH:
     682 <400> SEQUENCE: 48
E--> 684 Asn Ala Thr Tyr Lys Val Asp Val Ile....................Gln Arg Thr Arg Ser Lys
E--> 685 Pro
E--> 686 1.                5                 10
     689 <210> SEQ ID NO: 49
     690 <212> TYPE: PRT
     691 <213> ORGANISM: Homo sapiens
E--> 693 <211> LENGTH:
     693 <400> SEQUENCE: 49
     695 Asn Pro Thr Tyr Lys Met Tyr Glu Gly Gly Glu Pro Asp Asp Val Gly
```

same error in Seqs 39-40

← misaligned nos. (see item 3 on Error summary sheet)

same error in Seq 42-45

RAW SEQUENCE LISTING   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:51

Input Set : **A:\PTO.SS.TXT**   *same*
Output Set: **N:\CRF4\02012007\J595562.raw**

```
     696 1                 5                 10                15
E--> 699 Gly Leu Leu Asp Ala Asp Phe Ala Leu Asp Pro Asp..............Lys Pro Thr Asn
E--> 700                 20                25
E--> 703 Phe Thr Asn Pro
```

same error in seqs. 50-55, 57-59.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:52

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:31; Line(s) 465
Seq#:34; Line(s) 508
Seq#:48; Line(s) 684

VERIFICATION SUMMARY   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:52

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

```
L:12 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:54 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:57 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:1
L:92 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:95 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:7 SEQ:2
L:138 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:141 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:3
L:148 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:150 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:151 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:151 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:4
L:158 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:160 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:161 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:161 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:5
L:168 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:170 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:170 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:171 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:171 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:6
L:178 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:180 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:184 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:20 SEQ:7
L:192 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:194 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:195 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:195 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:8
L:202 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:204 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:205 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:208 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:9
L:216 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:218 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:219 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:222 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:10
L:230 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:232 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:233 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:236 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:11
L:244 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:246 M:333 E: Wrong sequence grouping, Amino acids not in groups!
```

VERIFICATION SUMMARY   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:52

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

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L:247 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:247 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:15 SEQ:12
L:254 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:256 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:257 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:257 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:13
L:264 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:266 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:267 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:267 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:14
L:274 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:276 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:277 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
M:332 Repeated in SeqNo=15
L:280 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:22 SEQ:15
L:288 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:290 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:291 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:291 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:16
L:298 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:300 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:304 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:17
L:312 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:318 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:318 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
L:318 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:22 SEQ:18
L:345 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:347 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:348 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:348 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:20
L:355 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:357 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:358 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:358 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:21
L:365 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:367 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:368 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:368 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:22
L:375 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:377 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:378 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:378 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:23
L:385 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:387 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:388 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
L:388 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:24
L:395 M:282 E: Numeric Field Identifier Missing, <211> is required.
```

VERIFICATION SUMMARY   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:52

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

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L:397 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:398 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:25
L:398 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:25
L:405 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:407 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
L:408 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:16 SEQ:26
L:415 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:417 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:418 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:418 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:13 SEQ:27
L:425 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:427 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:428 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
M:332 Repeated in SeqNo=28
L:431 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:21 SEQ:28
L:439 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:441 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:442 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
L:445 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:16 SEQ:29
L:453 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:455 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:456 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
L:456 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:30
L:463 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:465 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:469 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:469 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:17 SEQ:31
L:477 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:479 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:480 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:480 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:32
L:506 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:508 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:509 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
M:332 Repeated in SeqNo=34
L:513 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:21 SEQ:34
L:521 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:523 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:524 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:524 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:35
L:531 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:533 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:534 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:534 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:36
L:541 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:543 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:543 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
```

VERIFICATION SUMMARY   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:52

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

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L:544 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:37
L:551 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:553 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:557 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:557 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:561 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
M:332 Repeated in SeqNo=38
L:561 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:43 SEQ:38
L:568 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:570 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:571 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:39
L:578 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:580 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:581 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:40
L:588 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:594 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=41
L:594 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:26 SEQ:41
L:602 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:608 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:609 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:30 SEQ:42
L:616 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:622 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:623 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:623 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:31 SEQ:43
L:630 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:636 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:636 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:636 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:44
L:644 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:646 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:647 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:647 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:45
L:654 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:656 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:657 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:660 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:46
L:668 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:670 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:671 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
L:674 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:17 SEQ:47
L:682 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:684 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:686 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:15 SEQ:48
```

VERIFICATION SUMMARY   DATE: 02/01/2007
PATENT APPLICATION: US/10/595,562   TIME: 12:08:52

Input Set : **A:\PTO.SS.TXT**
Output Set: **N:\CRF4\02012007\J595562.raw**

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L:693 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:699 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:703 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:35 SEQ:49
L:711 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:717 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:717 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:50
L:725 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:731 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:731 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:51
L:739 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:741 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:742 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:52
L:751 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:761 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0
L:1072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0
```